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RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/10/016,686

TIME: 10:35:57

Input Set : A:\00069165.txt

Output Set: N:\CRF3\06052002\J016686.raw

ENTERED

3 <110> APPLICANT: Oxford Biomedica (UK) Limited
 4 Kingsman, Alan
 5 Kingsman, Susan Mary
 6 Bebbington, Christopher Robert
 7 Carrol, Miles William
 8 Ellard, Fiona Margaret
 9 Myers, Kevin Alan
 11 <120> TITLE OF INVENTION: Antibodies
 13 <130> FILE REFERENCE: 674523-2012
 15 <140> CURRENT APPLICATION NUMBER: 10/016,686
 C--> 16 <141> CURRENT FILING DATE: 2002-11-02
 18 <150> PRIOR APPLICATION NUMBER: PCT/GB00/04317
 19 <151> PRIOR FILING DATE: 2000-11-13
 21 <160> NUMBER OF SEQ ID NOS: 37
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 243
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: sequence of the mature secreted protein
 33 <400> SEQUENCE: 1
 35 Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala
 36 1 5 10 15
 39 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
 40 20 25 30
 43 Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 44 35 40 45
 47 Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn Gln Lys Phe
 48 50 55 60
 51 Lys Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 52 65 70 75 80
 55 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 56 85 90 95
 59 Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr Trp Gly Gln
 60 100 105 110
 63 Val Thr Ser Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 64 115 120 125
 67 Gly Thr Gly Gly Gly Gly Ser Ser Ile Val Met Thr Gln Thr Pro Thr
 68 130 135 140
 71 Phe Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala
 72 145 150 155 160
 75 Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly

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76          165          170          175
79 Gln Ser Pro Thr Leu Leu Ile Ser Tyr Thr Ser Ser Arg Tyr Ala Gly
80          180          185          190
83 Val Pro Asp Arg Phe Ile Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe
84          195          200          205
87 Thr Ile Ser Thr Leu Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln
88          210          215          220
91 Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu
92 225          230          235          240
95 Ile Lys Arg
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 68
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Cassette 1- Translation initiation signal and signal peptide
107 <400> SEQUENCE: 2
108 aagcttccac catgggatgg agctgtatca tcctcttctt ggtagcaaca gctacaggtg      60
110 tccactcc                                     68
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 488
115 <212> TYPE: PRT
116 <213> ORGANISM: Artificial Sequence
118 <220> FEATURE:
119 <223> OTHER INFORMATION: deduced amino acid sequence for the B7-1.5T4.1 fusion
protein
121 <400> SEQUENCE: 3
123 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
124 1          5          10          15
127 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
128          20          25          30
131 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
132          35          40          45
135 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
136          50          55          60
139 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
140 65          70          75          80
143 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
144          85          90          95
147 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
148          100          105          110
151 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
152          115          120          125
155 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
156          130          135          140
159 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
160 145          150          155          160
163 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
164          165          170          175
167 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp

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168          180          185          190
171 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
172          195          200          205
175 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
176          210          215          220
179 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
180 225          230          235          240
183 Asp Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Asp
184          245          250          255
187 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
188          260          265          270
191 Tyr Ser Phe Thr Gly Tyr Tyr Met His Trp Val Lys Gln Ser His Gly
192          275          280          285
195 Lys Ser Leu Glu Trp Ile Gly Arg Ile Asn Pro Asn Asn Gly Val Thr
196          290          295          300
199 Leu Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Leu Thr Val Asp Lys
200 305          310          315          320
203 Ser Ser Thr Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp
204          325          330          335
207 Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr Met Ile Thr Asn Tyr Val
208          340          345          350
211 Met Asp Tyr Trp Gly Gln Val Thr Ser Val Thr Val Ser Ser Gly Gly
212          355          360          365
215 Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Ser Ile Val
216          370          375          380
219 Met Thr Gln Thr Pro Thr Phe Leu Leu Val Ser Ala Gly Asp Arg Val
220 385          390          395          400
223 Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp
224          405          410          415
227 Tyr Gln Gln Lys Pro Gly Gln Ser Pro Thr Leu Leu Ile Ser Tyr Thr
228          420          425          430
231 Ser Ser Arg Tyr Ala Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Tyr
232          435          440          445
235 Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Leu Gln Ala Glu Asp Leu
236          450          455          460
239 Ala Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly
240 465          470          475          480
243 Gly Gly Thr Lys Leu Glu Ile Lys
244          485
247 <210> SEQ ID NO: 4
248 <211> LENGTH: 592
249 <212> TYPE: PRT
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: deduced amino acid sequence for the Ig-5T4 fusion protein
255 <400> SEQUENCE: 4
257 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
258 1          5          10          15
261 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys

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262		20		25		30										
265	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe
266			35					40					45			
269	Thr	Gly	Tyr	Tyr	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu
270		50					55					60				
273	Glu	Trp	Ile	Gly	Arg	Ile	Asn	Pro	Asn	Asn	Gly	Val	Thr	Leu	Tyr	Asn
274	65					70				75						80
277	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Ile	Leu	Thr	Val	Asp	Lys	Ser	Ser	Thr
278					85					90					95	
281	Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
282				100					105					110		
285	Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Met	Ile	Thr	Asn	Tyr	Val	Met	Asp	Tyr
286			115					120					125			
289	Trp	Gly	Gln	Val	Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
290		130					135					140				
293	Gly	Gly	Gly	Gly	Thr	Gly	Gly	Gly	Gly	Ser	Ser	Ile	Val	Met	Thr	Gln
294	145					150				155						160
297	Thr	Pro	Thr	Phe	Leu	Leu	Val	Ser	Ala	Gly	Asp	Arg	Val	Thr	Ile	Thr
298				165						170					175	
301	Cys	Lys	Ala	Ser	Gln	Ser	Val	Ser	Asn	Asp	Val	Ala	Trp	Tyr	Gln	Gln
302			180						185					190		
305	Lys	Pro	Gly	Gln	Ser	Pro	Thr	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Ser	Arg
306		195					200					205				
309	Tyr	Ala	Gly	Val	Pro	Asp	Arg	Phe	Ile	Gly	Ser	Gly	Tyr	Gly	Thr	Asp
310		210				215					220					
313	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Leu	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr
314	225				230					235						240
317	Phe	Cys	Gln	Gln	Asp	Tyr	Asn	Ser	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr
318				245						250					255	
321	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
322			260						265					270		
325	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
326		275					280					285				
329	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
330		290				295					300					
333	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
334	305				310					315						320
337	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Thr	Val	Pro	Ser	Ser	
338			325						330					335		
341	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
342		340					345					350				
345	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
346		355				360					365					
349	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
350		370				375					380					
353	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
354	385				390					395						400
357	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
358				405					410					415		

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361 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
362           420           425           430
365 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
366           435           440           445
369 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
370           450           455           460
373 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
374 465           470           475           480
377 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
378           485           490           495
381 Pro Pro Ser Arg Asp Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
382           500           505           510
385 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
386           515           520           525
389 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
390           530           535           540
393 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
394 545           550           555           560
397 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
398           565           570           575
401 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
402           580           585           590

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405 <210> SEQ ID NO: 5

406 <211> LENGTH: 729

407 <212> TYPE: DNA

408 <213> ORGANISM: Artificial Sequence

410 <220> FEATURE:

411 <223> OTHER INFORMATION: DNA sequence encoding a 5T4 ScFv designated 5T4ScFv.1

413 <400> SEQUENCE: 5

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414 gaggtccagc ttcagcagtc tggacctgac ctggtgaagc ctggggcttc agtgaagata      60
416 tcttgcaagg cttctggtta ctcattcact ggctactaca tgcactgggt gaagcagagc      120
418 catggaaaga gccttgagtg gattggacgt attaataccta acaatgggtg tactctctac      180
420 aaccagaaat tcaaggacaa ggccatatta actgtagaca agtcatccac cacagcctac      240
422 atggagctcc gcagcctgac atctgaggac tctgcggtct attactgtgc aagatctact      300
424 atgattacga actatgttat ggactactgg ggtcaagtaa cctcagtcac cgtctcctca      360
426 ggtggtggtg ggagcgggtg tggcggcact ggcggcggcg gatctagtat tgtgatgacc      420
428 cagactccca cattcctgct tgtttcagca ggagacaggg ttaccataac ctgcaaggcc      480
430 agtcagagtg tgagtaatga tgtagdttgg taccaacaga agccagggca gtctcctaca      540
432 ctgctcatat cctatacatc cagtcgctac gctggagtcc ctgacgctt cattggcagt      600
434 ggatatggga cggatttcac tttcaccatc agcactttgc aggctgaaga cctggcagtt      660
436 tatttctgtc agcaagatta taattctcct ccgacgttcg gtggaggcac caagctggaa      720
438 atcaaacgg                                     729

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441 <210> SEQ ID NO: 6

442 <211> LENGTH: 43

443 <212> TYPE: DNA

444 <213> ORGANISM: Artificial Sequence

446 <220> FEATURE:

447 <223> OTHER INFORMATION: oligonucleotide used to construct flexible linker to join
the ext

448 racellular domain of B7.1 and ScFv

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/016,686

DATE: 06/05/2002

TIME: 10:35:58

Input Set : A:\00069165.txt

Output Set: N:\CRF3\06052002\J016686.raw

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